

SEQUENCE LISTING

<110> Langenfeld, John
<120> BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS OF CANCER
<130> 54704.8036.US03
<150> US60/261,252
<151> 2001-01-12
<150> US10/044,716
<151> 2002-01-11
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<170> PatentIn version 3.2
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tgcccgacac `tgagacgctg ttcccagcgt gaaaagagag actgcgcggc cggcacccgg      180
gagaaggagg aggcaaagaa aaggaacgga cattcggtcc ttgcgccagg tcctttgacc      240
agagttttc catgtggacg ctcttcaat ggacgtgtcc ccgcgtgctt ctttagacgga      300
ctgcggtctc ctaaaggctcg acc atg gtg gcc ggg acc cgc tgt ctt cta gcg      353
                           Met Val Ala Gly Thr Arg Cys Leu Leu Ala
                           1           5           10
ttg ctg ctt ccc cag gtc ctc ctg ggc ggc gcg gct ggc ctc gtt ccg      401
Leu Leu Leu Pro Gln Val Leu Leu Gly Ala Ala Gly Leu Val Pro
                           15          20          25
gag ctg ggc cgc agg aag ttc gcg gcg tcg tcg ggc cgc ccc tca      449
Glu Leu Gly Arg Arg Lys Phe Ala Ala Ser Ser Gly Arg Pro Ser
                           30          35          40
tcc cag ccc tct gac gag gtc ctg agc gag ttc gag ttg cgg ctg ctc      497
Ser Gln Pro Ser Asp Glu Val Leu Ser Glu Phe Glu Leu Arg Leu Leu
                           45          50          55
agc atg ttc ggc ctg aaa cag aga ccc acc ccc agc agg gac gcc gtg      545
Ser Met Phe Gly Leu Lys Gln Arg Pro Thr Pro Ser Arg Asp Ala Val
                           60          65          70
gtg ccc ccc tac atg cta gac ctg tat cgc agg cac tca ggt cag ccg      593
Val Pro Pro Tyr Met Leu Asp Leu Tyr Arg Arg His Ser Gly Gln Pro
                           75          80          85          90
ggc tca ccc gcc cca gac cac cgg ttg gag agg gca gcc agc cga gcc      641
Gly Ser Pro Ala Pro Asp His Arg Leu Glu Arg Ala Ala Ser Arg Ala
                           95          100         105
aac act gtg cgc agc ttc cac cat gaa gaa tct ttg gaa gaa cta cca      689
Asn Thr Val Arg Ser Phe His His Glu Glu Ser Leu Glu Glu Leu Pro
                           110         115         120
gaa acg agt ggg aaa aca acc cgg aga ttc ttc ttt aat tta agt tct      737
Glu Thr Ser Gly Lys Thr Thr Arg Arg Phe Phe Phe Asn Leu Ser Ser

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att aat att tat gaa atc ata aaa cct gca aca gcc aac tcg aaa ttc Ile Asn Ile Tyr Glu Ile Lys Pro Ala Thr Ala Asn Ser Lys Phe 175	180	185	881
ccc gtg acc aga ctt ttg gac acc agg ttg gtg aat cag aat gca agc Pro Val Thr Arg Leu Leu Asp Thr Arg Leu Val Asn Gln Asn Ala Ser 190	195	200	929
agg tgg gaa agt ttt gat gtc acc ccc gct gtg atg cgg tgg act gca Arg Trp Glu Ser Phe Asp Val Thr Pro Ala Val Met Arg Trp Thr Ala 205	210	215	977
cag gga cac gcc aac cat gga ttc gtg gtg gaa gtg gcc cac ttg gag Gln Gly His Ala Asn His Gly Phe Val Val Glu Val Ala His Leu Glu 220	225	230	1025
gag aaa caa ggt gtc tcc aag aga cat gtt agg ata agc agg tct ttg Glu Lys Gln Gly Val Ser Lys Arg His Val Arg Ile Ser Arg Ser Leu 235	240	245	1073
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ttt ggc cat gat gga aaa ggg cat cct ctc cac aaa aga gaa aaa cgt Phe Gly His Asp Gly Lys Gly His Pro Leu His Lys Arg Glu Lys Arg 270	275	280	1169
caa gcc aaa cac aaa cag cgg aaa cgc ctt aag tcc agc tgt aag aga Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg 285	290	295	1217
cac cct ttg tac gtg gac ttc agt gac gtg ggg tgg aat gac tgg att His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile 300	305	310	1265
gtg gct ccc ccg ggg tat cac gcc ttt tac tgc cac gga gaa tgc cct Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro 315	320	325	1313
ttt cct ctg gct gat cat ctg aac tcc act aat cat gcc att gtt cag Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln 335	340	345	1361
acg ttg gtc aac tct gtt aac tct aag att cct aag gca tgc tgt gtc Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val 350	355	360	1409

ccg aca gaa ctc agt gct atc tcg atg ctg tac ctt gac gag aat gaa 1457
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 365 370 375

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Phe Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu
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Val Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys
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Gln Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu
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Asp Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp
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His Arg Leu Glu Arg Ala Ala .Ser Arg Ala Asn Thr Val Arg Ser Phe
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His His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr
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Thr Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe
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Ile Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala
145 150 155 160

Leu Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile
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Ile Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu
 180 185 190

Asp Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Ser Phe Asp
195 200 205

Val	Thr	Pro	Ala	Val	Met	Arg	Trp	Thr	Ala	Gln	Gly	His	Ala	Asn	His
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Gly Phe Val Val Glu Val Ala His Leu Glu Glu Lys Gln Gly Val Ser
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Lys Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser
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Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys
260 265 270

Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His Lys Gln
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Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp
290 295 300

Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr
 305 310 315 320

His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His
325 330 335

Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val
340 345 350

Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala
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<301> Valenzuela,D.M., Economides,A.N., Rojas,E., Lamb,T.M., Nunez,L.,
 Jones,P., Ip,N.Y., Espinosa,R., Brannan,C.I., Gilbert,D.J.,
 Copeland,N.G., Jenkins,N.A., LeBeau,M.M., Harland,R.M. and
 Yancopoulos,G.D.
<302> Identification of mammalian noggin and its expression in the
 adult nervous system
<303> J. Neurosci.
<304> 15
<305> 9
<306> 6077-6084
<307> 1995
<308> NM_005450
<309> 2000-11-01
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<300>
<301> McMahon,J.A., Takada,S., Zimmerman,L.B., Fan,C.M., Harland,R.M.
 and McMahon, A.P.
<302> Noggin-mediated antagonism of BMP signaling is required for
 growth and patterning of the neural tube and somite
<303> Genes Dev.
<304> 12
<305> 10
<306> 1438-1452
<307> 1998
<308> NM_005450
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<313> (1)..(699)

<300>
<301> Brunet,L.J., McMahon,J.A., McMahon,A.P. and Harland,R.M.
<302> Noggin, cartilage morphogenesis, and joint formation in the
 mammalian skeleton
<303> Science
<304> 280
<305> 5368
<306> 1455-1457
<307> 1998
<308> NM_005450
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<300>
<301> Smith, W.C.

<302> TGF beta inhibitors. New and unexpected requirements in
 vertebrate development
 <303> Trends Genet.
 <304> 15
 <305> 1
 <306> 3-5
 <307> 1999
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 <301> Gong,Y., Krakow,D., Marcelino,J., Wilkin,D., Chitayat,D.,
 Babul-Hirji,R., Hudgins,L., Cremers,C.W., Cremers,F.P.,
 Brunner,H.G., Reinker,K., Rimoin,D.L., Cohn,D.H., Goodman,F.R.,
 Reardon,W., Patton,M., Francomano,C.A. and Warman,M.L.
 <302> Heterozygous mutations in the gene encoding noggin affect human
 joint morphogenesis
 <303> Nat. Genet.
 <304> 21
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 <306> 302-304
 <307> 1999
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 Val Leu Gly Leu Arg Ala Thr Pro Ala Gly Gly Gln His Tyr Leu His
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atc cgc ccg gca ccc agc gac aac ctg ccc ctg gtg gac ctc atc gaa 144

Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu			
35	40	45	
cac cca gac cct atc ttt gac ccc aag gaa aag gat ctg aac gag acg			192
His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr			
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ctg ctg cgc tcg ctc ggg ggc cac tac gac cca ggc ttc atg gcc			240
Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala			
65	70	75	80
acc tcg ccc ccc gag gac cg ^g ccc ggc ggg ggc ggg ggt gca gct ggg			288
Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Ala Ala Gly			
85	90	95	
ggc gcg gag gac ctg gc ^g gag ctg gac cag ctg cgg cag cgg cc ^g			336
Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro			
100	105	110	
tcg ggg gcc atg cc ^g agc gag atc aaa ggg cta gag ttc tcc gag ggc			384
Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly			
115	120	125	
ttg gcc cag ggc aag aag cag cg ^c cta agc aag aag ctg cgg agg aag			432
Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys			
130	135	140	
tta cag atg tgg ctg tgg tcg cag aca ttc tgc ccc gtg ctg tac gc ^g			480
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145	150	155	160
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Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys			
180	185	190	
aag ccg tcc aag tcc gtg cac ctc acg gtg ctg cgg tgg cgc tgt cag			624
Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln			
195	200	205	
cg ^g cgc ggg ggc cag cg ^c tgc ggc tgg att ccc atc cag tac ccc atc			672
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															115
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															135
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Ile Arg Pro Ala Pro Ser Asp Asn Leu Pro Leu Val Asp Leu Ile Glu
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Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Gly Pro Ala Gly
85          90          95

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 130 135 140

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Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro
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Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly
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 <301> Millet, C., Lemaire, P., Orsetti, B., Guglielmi, P., and
 Francois, V.
 <302> The human chordin gene encodes several differentially expressed
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 <303> Mech. Dev.
 <304> 106
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 <301> Millet, C., and Francois, V.

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ctg ctg cgc tct agc ctc cgc ttc tct atc tcc tac agg cgg ctg gac Leu Leu Arg Ser Leu Arg Phe Ser Ile Ser Tyr Arg Arg Leu Asp	195 200	205	864
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cat gtg gca ctt gtg aca ctc act cac cct tca ggg gag gtc tgg ggg His Val Ala Leu Val Thr Leu Thr His Pro Ser Gly Glu Val Trp Gly	255 260	265	1056 270
cct ctc atc cgg cac cgg gcc ctg gct gca gag acc ttc agt gcc atc Pro Leu Ile Arg His Arg Ala Leu Ala Ala Glu Thr Phe Ser Ala Ile	275 280	285	1104
ctg act cta gaa ggc ccc cca cag cag ggc gta ggg ggc atc acc ctg Leu Thr Leu Glu Gly Pro Pro Gln Gln Gly Val Gly Gly Ile Thr Leu	290 295	300	1152
ctc act ctc agt gac aca gag gac tcc ttg cat ttt ttg ctg ctc ttc Leu Thr Leu Ser Asp Thr Glu Asp Ser Leu His Phe Leu Leu Leu Phe	305 310	315	1200

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cac acg gcc gtg ggt atc tgc cct ggg ctg ggt gcc cga ggg gct cat His Thr Ala Val Gly Ile Cys Pro Gly Leu Gly Ala Arg Gly Ala His 480 485 490	1728
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ccg gtg cag gct ccc gac cag tgc tgc cct gtt tgc cct gag aaa caa Pro Val Gln Ala Pro Asp Gln Cys Cys Pro Val Cys Pro Glu Lys Gln 755 760 765	2544
gat gtc aga gac ttg cca ggg ctg cca agg agc ccg gac cca gga gag	2592

Asp Val Arg Asp Leu Pro Gly Leu Pro Arg Ser Arg Asp Pro Gly Glu			
770	775	780	
ggc tgc tat ttt gat ggt gac cgg agc tgg cgg gca gcg ggt acg cgg			2640
Gly Cys Tyr Phe Asp Gly Asp Arg Ser Trp Arg Ala Ala Gly Thr Arg			
785	790	795	
tgg cac ccc gtt gtg ccc ccc ttt ggc tta att aag tgt gct gtc tgc			2688
Trp His Pro Val Val Pro Pro Phe Gly Leu Ile Lys Cys Ala Val Cys			
800	805	810	
acc tgc aag ggg ggc act gga gag gtg cac tgt gag aag gtg cag tgt			2736
Thr Cys Lys Gly Gly Thr Gly Glu Val His Cys Glu Lys Val Gln Cys			
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ccc cgg ctg gcc tgt gcc cag cct gtg cgt gtc aac ccc acc gac tgc			2784
Pro Arg Leu Ala Cys Ala Gln Pro Val Arg Val Asn Pro Thr Asp Cys			
835	840	845	
tgc aaa cag tgt cca gtg ggg tcg ggg gcc cac ccc cag ctg ggg gac			2832
Cys Lys Gln Cys Pro Val Gly Ser Gly Ala His Pro Gln Leu Gly Asp			
850	855	860	
ccc atg cag gct gat ggg ccc cgg ggc tgc cgt ttt gct ggg cag tgg			2880
Pro Met Gln Ala Asp Gly Pro Arg Gly Cys Arg Phe Ala Gly Gln Trp			
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ttc cca gag agt cag agc tgg cac ccc tca gtg ccc cct ttt gga gag			2928
Phe Pro Glu Ser Gln Ser Trp His Pro Ser Val Pro Pro Phe Gly Glu			
880	885	890	
atg agc tgt atc acc tgc aga tgt ggg gca ggg gtg cct cac tgt gag			2976
Met Ser Cys Ile Thr Cys Arg Cys Gly Ala Gly Val Pro His Cys Glu			
895	900	905	910
cgg gat gac tgt tca ctg cca ctg tcc tgt ggc tcg ggg aag gag agt			3024
Arg Asp Asp Cys Ser Leu Pro Leu Ser Cys Gly Ser Gly Lys Glu Ser			
915	920	925	
cga tgc tgt tcc cgc tgc acg gcc cac cgg cgg cca gcc cca gag acc			3072
Arg Cys Cys Ser Arg Cys Thr Ala His Arg Arg Pro Ala Pro Glu Thr			
930	935	940	
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Arg Thr Asp Pro Glu Leu Glu Ala Glu Gly Ser			
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aaaaaaaaaa aaa	3547

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	30

Val Leu Pro Ile Arg Ser Glu Lys Glu Pro Leu Pro Val Arg Gly Ala	
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Ala Gly Cys Thr Phe Gly Gly Lys Val Tyr Ala Leu Asp Glu Thr Trp	
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	60

His Pro Asp Leu Gly Glu Pro Phe Gly Val Met Arg Cys Val Leu Cys	
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	75
	80

Ala Cys Glu Ala Pro Gln Trp Gly Arg Arg Thr Arg Gly Pro Gly Arg	
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	95

Val Ser Cys Lys Asn Ile Lys Pro Glu Cys Pro Thr Pro Ala Cys Gly	
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	110

Gln Pro Arg Gln Leu Pro Gly His Cys Cys Gln Thr Cys Pro Gln Glu	
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	125

Arg Ser Ser Ser Glu Arg Gln Pro Ser Gly Leu Ser Phe Glu Tyr Pro	
130	135
	140

Arg Asp Pro Glu His Arg Ser Tyr Ser Asp Arg Gly Glu Pro Gly Ala	
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	155
	160

Glu Glu Arg Ala Arg Gly Asp Gly His Thr Asp Phe Val Ala Leu Leu	
165	170
	175

Thr Gly Pro Arg Ser Gln Ala Val Ala Arg Ala Arg Val Ser Leu Leu
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Arg Ser Ser Leu Arg Phe Ser Ile Ser Tyr Arg Arg Leu Asp Arg Pro
 195 200 205

Thr Arg Ile Arg Phe Ser Asp Ser Asn Gly Ser Val Leu Phe Glu His
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Pro Ala Ala Pro Thr Gln Asp Gly Leu Val Cys Gly Val Trp Arg Ala
 225 230 235 240

Val Pro Arg Leu Ser Leu Arg Leu Leu Arg Ala Glu Gln Leu His Val
 245 250 255

Ala Leu Val Thr Leu Thr His Pro Ser Gly Glu Val Trp Gly Pro Leu
 260 265 270

Ile Arg His Arg Ala Leu Ala Ala Glu Thr Phe Ser Ala Ile Leu Thr
 275 280 285

Leu Glu Gly Pro Pro Gln Gln Gly Val Gly Gly Ile Thr Leu Leu Thr
 290 295 300

Leu Ser Asp Thr Glu Asp Ser Leu His Phe Leu Leu Leu Phe Arg Gly
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Leu Leu Glu Pro Arg Ser Gly Gly Leu Thr Gln Val Pro Leu Arg Leu
 325 330 335

Gln Ile Leu His Gln Gly Gln Leu Leu Arg Glu Leu Gln Ala Asn Val
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Ser Ala Gln Glu Pro Gly Phe Ala Glu Val Leu Pro Asn Leu Thr Val
 355 360 365

Gln Glu Met Asp Trp Leu Val Leu Gly Glu Leu Gln Met Ala Leu Glu
 370 375 380

Trp Ala Gly Arg Pro Gly Leu Arg Ile Ser Gly His Ile Ala Ala Arg
 385 390 395 400

Lys Ser Cys Asp Val Leu Gln Ser Val Leu Cys Gly Ala Asp Ala Leu
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Ile Pro Val Gln Thr Gly Ala Ala Gly Ser Ala Ser Leu Thr Leu Leu
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Gly Asn Gly Ser Leu Ile Tyr Gln Val Gln Val Val Gly Thr Ser Ser
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Glu Val Val Ala Met Thr Leu Glu Thr Lys Pro Gln Arg Arg Asp Gln
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Arg Thr Val Leu Cys His Met Ala Gly Leu Gln Pro Gly Gly His Thr
 465 470 475 480

Ala Val Gly Ile Cys Pro Gly Leu Gly Ala Arg Gly Ala His Met Leu
 485 490 495

Leu Gln Asn Glu Leu Phe Leu Asn Val Gly Thr Lys Asp Phe Pro Asp
 500 505 510

Gly Glu Leu Arg Gly His Val Ala Ala Leu Pro Tyr Cys Gly His Ser
 515 520 525

Ala Arg His Asp Thr Leu Pro Val Pro Leu Ala Gly Ala Leu Val Leu
 530 535 540

Pro Pro Val Lys Ser Gln Ala Ala Gly His Ala Trp Leu Ser Leu Asp
 545 550 555 560

Thr His Cys His Leu His Tyr Glu Val Leu Leu Ala Gly Leu Gly Gly
 565 570 575

Ser Glu Gln Gly Thr Val Thr Ala His Leu Leu Gly Pro Pro Gly Thr
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Pro Gly Pro Arg Arg Leu Leu Lys Gly Phe Tyr Gly Ser Glu Ala Gln
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Gly Val Val Lys Asp Leu Glu Pro Glu Leu Leu Arg His Leu Ala Lys
 610 615 620

Gly Met Ala Ser Leu Leu Ile Thr Thr Lys Gly Ser Pro Arg Gly Glu

625	630	635	640
Leu Arg Gly Gln Val His Ile Ala Asn Gln Cys Glu Val Gly Gly Leu			
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Arg Leu Glu Ala Ala Gly Ala Glu Gly Val Arg Ala Leu Gly Ala Pro			
660	665		670
Asp Thr Ala Ser Ala Ala Pro Pro Val Val Pro Gly Leu Pro Ala Leu			
675	680		685
Ala Pro Ala Lys Pro Gly Gly Pro Gly Arg Pro Arg Asp Pro Asn Thr			
690	695		700
Cys Phe Phe Glu Gly Gln Gln Arg Pro His Gly Ala Arg Trp Ala Pro			
705	710	715	720
Asn Tyr Asp Pro Leu Cys Ser Leu Cys Thr Cys Gln Arg Arg Thr Val			
725	730		735
Ile Cys Asp Pro Val Val Cys Pro Pro Pro Ser Cys Pro His Pro Val			
740	745		750
Gln Ala Pro Asp Gln Cys Cys Pro Val Cys Pro Glu Lys Gln Asp Val			
755	760	765	
Arg Asp Leu Pro Gly Leu Pro Arg Ser Arg Asp Pro Gly Glu Gly Cys			
770	775	780	
Tyr Phe Asp Gly Asp Arg Ser Trp Arg Ala Ala Gly Thr Arg Trp His			
785	790	795	800
Pro Val Val Pro Pro Phe Gly Leu Ile Lys Cys Ala Val Cys Thr Cys			
805	810		815
Lys Gly Gly Thr Gly Glu Val His Cys Glu Lys Val Gln Cys Pro Arg			
820	825	830	
Leu Ala Cys Ala Gln Pro Val Arg Val Asn Pro Thr Asp Cys Cys Lys			
835	840	845	
Gln Cys Pro Val Gly Ser Gly Ala His Pro Gln Leu Gly Asp Pro Met			
850	855	860	

Gln Ala Asp Gly Pro Arg Gly Cys Arg Phe Ala Gly Gln Trp Phe Pro
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Glu Ser Gln Ser Trp His Pro Ser Val Pro Pro Phe Gly Glu Met Ser
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Cys Ile Thr Cys Arg Cys Gly Ala Gly Val Pro His Cys Glu Arg Asp
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Asp Cys Ser Leu Pro Leu Ser Cys Gly Ser Gly Lys Glu Ser Arg Cys
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<301> Topol, L.Z., Modi, W.S., Koochekpour, S., and Blair, D.G.
<302> DRM/Gremlin (CKTSF1B1) maps to human chromosome 15 and is highly
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<303> Cytogenet. Cell Genet.
<304> 89
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<301> Topol, L.Z., Marx, M., Calothy, G., and Blair, D.G.
<302> Direct Submission
<303> Oncogene Mechanisms Section, Basic Research Laboratory, NIH/NCI
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actgacagt atg agc cgc aca gcc tac acg gtg gga gcc ctg ctt ctc ctc      171
    Met Ser Arg Thr Ala Tyr Thr Val Gly Ala Leu Leu Leu Leu
    1           5           10

ttg ggg acc ctg ctg ccg gct gct gaa ggg aaa aag aaa ggg tcc caa      219
Leu Gly Thr Leu Leu Pro Ala Ala Glu Gly Lys Lys Lys Gly Ser Gln
15          20          25          30

ggt gcc atc ccc ccg cca gac aag gcc cag cac aat gac tca gag cag      267
Gly Ala Ile Pro Pro Asp Lys Ala Gln His Asn Asp Ser Glu Gln
35          40          45

act cag tcg ccc cag cag cct ggc tcc agg aac cgg ggg cgg ggc caa      315
Thr Gln Ser Pro Gln Gln Pro Gly Ser Arg Asn Arg Gly Arg Gly Gln
50          55          60

ggg cgg ggc act gcc atg ccc ggg gag gag gtg ctg gag tcc agc caa      363
Gly Arg Gly Thr Ala Met Pro Gly Glu Glu Val Leu Glu Ser Ser Gln
65          70          75

gag gcc ctg cat gtg acg gag cgc aaa tac ctg aag cga gac tgg tgc      411
Glu Ala Leu His Val Thr Glu Arg Lys Tyr Leu Lys Arg Asp Trp Cys
80          85          90

aaa acc cag ccg ctt aag cag acc atc cac gag gaa ggc tgc aac agt      459
Lys Thr Gln Pro Leu Lys Gln Thr Ile His Glu Glu Gly Cys Asn Ser
95          100         105         110

cgc acc atc atc aac cgc ttc tgt tac ggc cag tgc aac tct ttc tac      507
Arg Thr Ile Ile Asn Arg Phe Cys Tyr Gly Gln Cys Asn Ser Phe Tyr
115         120         125

atc ccc agg cac atc cgg aag gag gaa ggt tcc ttt cag tcc tgc tcc      555
Ile Pro Arg His Ile Arg Lys Glu Glu Gly Ser Phe Gln Ser Cys Ser
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ttc tgc aag ccc aag aaa ttc act acc atg atg gtc aca ctc aac tgc      603

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Ile Pro Pro Pro Asp Lys Ala Gln His Asn Asp Ser Glu Gln Thr Gln
 35 40 45

Ser Pro Gln Gln Pro Gly Ser Arg Asn Arg Gly Arg Gly Gln Gly Arg
 50 55 60

Gly Thr Ala Met Pro Gly Glu Glu Val Leu Glu Ser Ser Gln Glu Ala
 65 70 75 80

Leu His Val Thr Glu Arg Lys Tyr Leu Lys Arg Asp Trp Cys Lys Thr
 85 90 95

Gln Pro Leu Lys Gln Thr Ile His Glu Glu Gly Cys Asn Ser Arg Thr
 100 105 110

Ile Ile Asn Arg Phe Cys Tyr Gly Gln Cys Asn Ser Phe Tyr Ile Pro
 115 120 125

Arg His Ile Arg Lys Glu Glu Gly Ser Phe Gln Ser Cys Ser Phe Cys
 130 135 140

Lys Pro Lys Lys Phe Thr Thr Met Met Val Thr Leu Asn Cys Pro Glu
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Leu Gln Pro Pro Thr Lys Lys Arg Val Thr Arg Val Lys Gln Cys
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Arg Cys Ile Ser Ile Asp Leu Asp
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<301> Lah, M., Brodnicki, T., Maccarone, P., Nash, A., Stanley, E., and
 Harvey, R.P.
<302> Human cerberus related gene CER1 maps to chromosome 9
<303> Genomics
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1           5               10              15

acc aca cgg cac cag gat ggc cgc cag aat cag agt tct ctt tcc ccc      96
Thr Thr Arg His Gln Asp Gly Arg Gln Asn Gln Ser Ser Leu Ser Pro
20          25              30

gta ctc ctg cca agg aatcaa aga gag ctt ccc aca ggc aac cat gag      144
Val Leu Pro Arg Asn Gln Arg Glu Leu Pro Thr Gly Asn His Glu
35          40              45

gaa gct gag gag aag cca gat ctg ttt gtc gca gtg cca cac ctt gta      192
Glu Ala Glu Glu Lys Pro Asp Leu Phe Val Ala Val Pro His Leu Val
50          55              60

gcc acc agc cct gca ggg gaa ggc cag agg cag aga gag aag atg ctg      240
Ala Thr Ser Pro Ala Gly Glu Gly Gln Arg Gln Arg Glu Lys Met Leu
65          70              75              80

tcc aga ttt ggc agg ttc tgg aag aag cct gag aga gaa atg cat cca      288
Ser Arg Phe Gly Arg Phe Trp Lys Lys Pro Glu Arg Glu Met His Pro
85          90              95

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Ser Arg Asp Ser Asp Ser Glu Pro Phe Pro Pro Gly Thr Gln Ser Leu	
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atc cag ccg ata gat gga atg aaa atg gag aaa tct cct ctt cgaa gaa	384
Ile Gln Pro Ile Asp Gly Met Lys Met Glu Lys Ser Pro Leu Arg Glu	
115 120 125	
gaa gcc aag aaa ttc tgg cac cac ttc atg ttc aga aaa act ccg gct	432
Glu Ala Lys Lys Phe Trp His His Phe Met Phe Arg Lys Thr Pro Ala	
130 135 140	
tct cag ggg gtc atc ttg ccc atc aaa agc cat gaa gta cat tgg gag	480
Ser Gln Gly Val Ile Leu Pro Ile Lys Ser His Glu Val His Trp Glu	
145 150 155 160	
acc tgc agg aca gtg ccc ttc agc cag act ata acc cac gaa ggc tgt	528
Thr Cys Arg Thr Val Pro Phe Ser Gln Thr Ile Thr His Glu Gly Cys	
165 170 175	
gaa aaa gta gtt gtt cag aac aac ctt tgc ttt ggg aaa tgc ggg tct	576
Glu Lys Val Val Val Gln Asn Asn Leu Cys Phe Gly Lys Cys Gly Ser	
180 185 190	
gtt cat ttt cct gga gcc gcg cag cac tcc cat acc tcc tgc tct cac	624
Val His Phe Pro Gly Ala Ala Gln His Ser His Thr Ser Cys Ser His	
195 200 205	
tgt ttg cct gcc aag ttc acc acg atg cac ttg cca ctg aac tgc act	672
Cys Leu Pro Ala Lys Phe Thr Thr Met His Leu Pro Leu Asn Cys Thr	
210 215 220	
gaa ctt tcc tcc gtg atc aag gtg gtg atg ctg gtg gag gag tgc cag	720
Glu Leu Ser Ser Val Ile Lys Val Val Met Leu Val Glu Glu Cys Gln	
225 230 235 240	
tgc aag gtg aag acg gag cat gaa gat gga cac atc cta cat gct ggc	768
Cys Lys Val Lys Thr Glu His Glu Asp Gly His Ile Leu His Ala Gly	
245 250 255	
tcc cag gat tcc ttt atc cca gga gtt tca gct tga	804
Ser Gln Asp Ser Phe Ile Pro Gly Val Ser Ala	
260 265	

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Thr Thr Arg His Gln Asp Gly Arg Gln Asn Gln Ser Ser Leu Ser Pro
 20 25 30

Val Leu Leu Pro Arg Asn Gln Arg Glu Leu Pro Thr Gly Asn His Glu
 35 40 45

Glu Ala Glu Glu Lys Pro Asp Leu Phe Val Ala Val Pro His Leu Val
 50 55 60

Ala Thr Ser Pro Ala Gly Glu Gly Gln Arg Gln Arg Glu Lys Met Leu
 65 70 75 80

Ser Arg Phe Gly Arg Phe Trp Lys Lys Pro Glu Arg Glu Met His Pro
 85 90 95

Ser Arg Asp Ser Asp Ser Glu Pro Phe Pro Pro Gly Thr Gln Ser Leu
 100 105 110

Ile Gln Pro Ile Asp Gly Met Lys Met Glu Lys Ser Pro Leu Arg Glu
 115 120 125

Glu Ala Lys Lys Phe Trp His His Phe Met Phe Arg Lys Thr Pro Ala
 130 135 140

Ser Gln Gly Val Ile Leu Pro Ile Lys Ser His Glu Val His Trp Glu
 145 150 155 160

Thr Cys Arg Thr Val Pro Phe Ser Gln Thr Ile Thr His Glu Gly Cys
 165 170 175

Glu Lys Val Val Val Gln Asn Asn Leu Cys Phe Gly Lys Cys Gly Ser
 180 185 190

Val His Phe Pro Gly Ala Ala Gln His Ser His Thr Ser Cys Ser His
 195 200 205

Cys Leu Pro Ala Lys Phe Thr Thr Met His Leu Pro Leu Asn Cys Thr
 210 215 220

Glu Leu Ser Ser Val Ile Lys Val Val Met Leu Val Glu Glu Cys Gln
 225 230 235 240

Cys Lys Val Lys Thr Glu His Glu Asp Gly His Ile Leu His Ala Gly

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255

Ser Gln Asp Ser Phe Ile Pro Gly Val Ser Ala
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 <301> ten Dijke, P., Yamashita, H., Ichijo, H., Franzen, P., Laiho, M., Miyazono, K., and Heldin, C.H.
 <302> Characterization of type I receptors for transforming growth factor-beta and activin
 <303> Science
 <304> 264
 <305> 5155
 <306> 101-104
 <307> 1994
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 <302> Cloning of human bone morphogenetic protein type IB receptor (BMPR-IB) and its expression in prostate cancer in comparison with other BMPRs
 <303> Oncogene
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 <306> 1377-1382
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 <302> Assignment of the BMPR1A and BMPR1B genes to human chromosome 10q22.3 and 4q23-->q24 by in situ hybridization and radiation hybrid mapping
 <303> Cytogenet. Cell. Genet.
 <304> 81
 <305> 3
 <306> 285-286
 <307> 1998
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<301> Astrom, A.K., Jin, D., Immura, T., Roijer, E., Rosenzweig, B.,
 Miyazono, K., ten Dijke, P., and Stenman, G.
 <302> Chromosomal localization of three human genes encoding bone
 morphogenetic protein receptors
 <303> Mamm. Genome
 <304> 10
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 gtgaaaaggaa aggaagatca tttcatgcct tggtgataaa gtttcagact tctgctgatt 180
 cataaccatt tggctctgag ctatgacaag agagggaaaca aaaagttaaa cttacaagcc 240

tgccataagt gagaagcaaa cttccttgc aac atg ctt ttg cga agt gca gga Met Leu Leu Arg Ser Ala Gly 1 5	294
aaa tta aat gtg ggc acc aag aaa gag gat ggt gag agt aca gcc ccc Lys Leu Asn Val Gly Thr Lys Lys Glu Asp Gly Glu Ser Thr Ala Pro 10 15 20	342
acc ccc cgt cca aag gtc ttg cgt tgt aaa tgc cac cac cat tgt cca Thr Pro Arg Pro Lys Val Leu Arg Cys Lys Cys His His His Cys Pro 25 30 35	390
gaa gac tca gtc aac aat att tgc agc aca gac gga tat tgt ttc acg Glu Asp Ser Val Asn Asn Ile Cys Ser Thr Asp Gly Tyr Cys Phe Thr 40 45 50 55	438
atg ata gaa gag gat gac tct ggg ttg cct gtg gtc act tct ggt tgc Met Ile Glu Glu Asp Asp Ser Gly Leu Pro Val Val Thr Ser Gly Cys 60 65 70	486
cta gga cta gaa ggc tca gat ttt cag tgt cgg gac act ccc att cct Leu Gly Leu Glu Gly Ser Asp Phe Gln Cys Arg Asp Thr Pro Ile Pro 75 80 85	534
cat caa aga aga tca att gaa tgc tgc aca gaa agg aac gaa tgt aat His Gln Arg Arg Ser Ile Glu Cys Cys Thr Glu Arg Asn Glu Cys Asn 90 95 100	582
aaa gac cta cac cct aca ctg cct cca ttg aaa aac aga gat ttt gtt Lys Asp Leu His Pro Thr Leu Pro Pro Leu Lys Asn Arg Asp Phe Val 105 110 115	630
gat gga cct ata cac cac agg gct tta ctt ata tct gtg act gtc tgt Asp Gly Pro Ile His His Arg Ala Leu Leu Ile Ser Val Thr Val Cys 120 125 130 135	678
agt ttg ctc ttg gtc ctt atc ata tta ttt tgt tac ttc cgg tat aaa Ser Leu Leu Leu Val Leu Ile Ile Leu Phe Cys Tyr Phe Arg Tyr Lys 140 145 150	726
aga caa gaa acc aga cct cga tac agc att ggg tta gaa cag gat gaa Arg Gln Glu Thr Arg Pro Arg Tyr Ser Ile Gly Leu Glu Gln Asp Glu 155 160 165	774
act tac att cct cct gga gaa tcc ctg aga gac tta att gag cag tct Thr Tyr Ile Pro Pro Gly Glu Ser Leu Arg Asp Leu Ile Glu Gln Ser 170 175 180	822
cag agc tca gga agt gga tca ggc ctc cct ctg gtc caa agg act Gln Ser Ser Gly Ser Gly Ser Gly Leu Pro Leu Leu Val Gln Arg Thr 185 190 195	870
ata gct aag cag att cag atg gtg aaa cag att gga aaa ggt cgc tat Ile Ala Lys Gln Ile Gln Met Val Lys Gln Ile Gly Lys Gly Arg Tyr 200 205 210 215	918

ggg gaa gtt tgg atg gga aag tgg cgt ggc gaa aag gta gct gtg aaa Gly Glu Val Trp Met Gly Lys Trp Arg Gly Glu Lys Val Ala Val Lys 220 225 230	966
gtg ttc ttc acc aca gag gaa gcc agc tgg ttc aga gag aca gaa ata Val Phe Phe Thr Thr Glu Glu Ala Ser Trp Phe Arg Glu Thr Glu Ile 235 240 245	1014
tat cag aca gtg ttg atg agg cat gaa aac att ttg ggt ttc att gct Tyr Gln Thr Val Leu Met Arg His Glu Asn Ile Leu Gly Phe Ile Ala 250 255 260	1062
gca gat atc aaa ggg aca ggg tcc tgg acc cag ttg tac cta atc aca Ala Asp Ile Lys Gly Thr Gly Ser Trp Thr Gln Leu Tyr Leu Ile Thr 265 270 275	1110
gac tat cat gaa aat ggt tcc ctt tat gat tat ctg aag tcc acc acc Asp Tyr His Glu Asn Gly Ser Leu Tyr Asp Tyr Leu Lys Ser Thr Thr 280 285 290 295	1158
cta gac gct aaa tca atg ctg aag tta gcc tac tct tct gtc agt ggc Leu Asp Ala Lys Ser Met Leu Lys Leu Ala Tyr Ser Ser Val Ser Gly 300 305 310	1206
tta tgt cat tta cac aca gaa atc ttt agt act caa ggc aaa cca gca Leu Cys His Leu His Thr Glu Ile Phe Ser Thr Gln Gly Lys Pro Ala 315 320 325	1254
att gcc cat cga gat ctg aaa agt aaa aac att ctg gtc aag aaa aat Ile Ala His Arg Asp Leu Lys Ser Lys Asn Ile Leu Val Lys Lys Asn 330 335 340	1302
gga act tgc tgt att gct gac ctg ggc ctg gct gtt aaa ttt att agt Gly Thr Cys Cys Ile Ala Asp Leu Gly Leu Ala Val Lys Phe Ile Ser 345 350 355	1350
gat aca aat gaa gtt gac ata cca cct aac act cga gtt ggc acc aaa Asp Thr Asn Glu Val Asp Ile Pro Pro Asn Thr Arg Val Gly Thr Lys 360 365 370 375	1398
cgc tat atg cct cca gaa gtg ttg gac gag agc ttg aac aga aat cac Arg Tyr Met Pro Pro Glu Val Leu Asp Glu Ser Leu Asn Arg Asn His 380 385 390	1446
ttc cag tct tac atc atg gct gac atg tat agt ttt ggc ctc atc ctt Phe Gln Ser Tyr Ile Met Ala Asp Met Tyr Ser Phe Gly Leu Ile Leu 395 400 405	1494
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20								25						30	

Lys Cys His His His Cys Pro Glu Asp Ser Val Asn Asn Ile Cys Ser
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Thr Asp Gly Tyr Cys Phe Thr Met Ile Glu Glu Asp Asp Ser Gly Leu
50 55 60

Pro	Val	Val	Thr	Ser	Gly	Cys	Leu	Gly	Leu	Glu	Gly	Ser	Asp	Phe	Gln
65					70					75					80

Cys Arg Asp Thr Pro Ile Pro His Gln Arg Arg Ser Ile Glu Cys Cys
85 90 95

Thr Glu Arg Asn Glu Cys Asn Lys Asp Leu His Pro Thr Leu Pro Pro
 100 105 110

Leu Lys Asn Arg Asp Phe Val Asp Gly Pro Ile His His Arg Ala Leu
 115 120 125

Leu Ile Ser Val Thr Val Cys Ser Leu Leu Leu Val Leu Ile Ile Leu
 130 135 140

Phe Cys Tyr Phe Arg Tyr Lys Arg Gln Glu Thr Arg Pro Arg Tyr Ser
 145 150 155 160

Ile Gly Leu Glu Gln Asp Glu Thr Tyr Ile Pro Pro Gly Glu Ser Leu
 165 170 175

Arg Asp Leu Ile Glu Gln Ser Gln Ser Ser Gly Ser Gly Ser Gly Leu
 180 185 190

Pro Leu Leu Val Gln Arg Thr Ile Ala Lys Gln Ile Gln Met Val Lys
 195 200 205

Gln Ile Gly Lys Gly Arg Tyr Gly Glu Val Trp Met Gly Lys Trp Arg
 210 215 220

Gly Glu Lys Val Ala Val Lys Val Phe Phe Thr Thr Glu Glu Ala Ser
 225 230 235 240

Trp Phe Arg Glu Thr Glu Ile Tyr Gln Thr Val Leu Met Arg His Glu
 245 250 255

Asn Ile Leu Gly Phe Ile Ala Ala Asp Ile Lys Gly Thr Gly Ser Trp
 260 265 270

Thr Gln Leu Tyr Leu Ile Thr Asp Tyr His Glu Asn Gly Ser Leu Tyr
 275 280 285

Asp Tyr Leu Lys Ser Thr Thr Leu Asp Ala Lys Ser Met Leu Lys Leu
 290 295 300

Ala Tyr Ser Ser Val Ser Gly Leu Cys His Leu His Thr Glu Ile Phe
 305 310 315 320

Ser Thr Gln Gly Lys Pro Ala Ile Ala His Arg Asp Leu Lys Ser Lys

325

330

335

Asn Ile Leu Val Lys Lys Asn Gly Thr Cys Cys Ile Ala Asp Leu Gly
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Leu Ala Val Lys Phe Ile Ser Asp Thr Asn Glu Val Asp Ile Pro Pro
 355 360 365

Asn Thr Arg Val Gly Thr Lys Arg Tyr Met Pro Pro Glu Val Leu Asp
 370 375 380

Glu Ser Leu Asn Arg Asn His Phe Gln Ser Tyr Ile Met Ala Asp Met
 385 390 395 400

Tyr Ser Phe Gly Leu Ile Leu Trp Glu Val Ala Arg Arg Cys Val Ser
 405 410 415

Gly Gly Ile Val Glu Glu Tyr Gln Leu Pro Tyr His Asp Leu Val Pro
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Ser Asp Pro Ser Tyr Glu Asp Met Arg Glu Ile Val Cys Ile Lys Lys
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Leu Arg Pro Ser Phe Pro Asn Arg Trp Ser Ser Asp Glu Cys Leu Arg
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Gln Met Gly Lys Leu Met Thr Glu Cys Trp Ala His Asn Pro Ala Ser
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